



10049710.090402

SEQUENCE LISTING

<110> SH Atsuhiko

Kato, Kou

Yamada, Yasuhiro

Nihira, Takuya

Shindo, Takuya

<120> METHOD FOR INDUCTION OF GENE EXPRESSION IN PLANT AND PLANT TREATED THEREBY

<130> 5405/18

<140> 10/049,710

<141> 2002-02-15

<150> PCT/JP01/05096

<151> 2001-06-15

<150> JP 2000-180466

<151> 2000-06-15

<160> 11

<170> PatentIn version 3.1

<210> 1

<211> 699

<212> DNA

<213> Streptomyces virginiae

<220>

<221> CDS

<222> (1)..(699)

<223>

<300>

<301> Okamoto, S., Nakamura, K., Nihira, T. and Yamada, Y.

<302> Virginiae butanolide binding protein from Streptomyces virginiae. Evidence that VbrA is not the virginiae butanolide binding protein and re-identification of the true binding protein

<303> Journal of Biological Chemistry

<304> 270

<305> 20

<306> 12319-12326

<307> 1995-05-19

<308> D32251

<309> 1994-07-19

<313> (1) .. (699)

<300>

<301> Okamoto, S., Nakamura, K., Nihira, T. and Yamada, Y.

<302> Virginiae butanolide binding protein from Streptomyces virginiae.  
Evidence that VbrA is not the virginiae butanolide binding protein and re-  
identification of the true binding protein

<303> Journal of Biological Chemistry

<304> 270

<305> 20

<306> 12319-12326

<307> 1995-05-19

<308> D32251

<309> 1994-07-19

<400> 1

atg gca gtg cga cac gaa cgg gtg gca gtg cga cag gaa cgg gcc gtc 48  
Met Ala Val Arg His Glu Arg Val Ala Val Arg Gln Glu Arg Ala Val  
1 5 10 15

cgc acg cgg cag gcg atc gtg cgg gca gcc gcc tcg gtc ttc gac gag 96

Arg Thr Arg Gln Ala Ile Val Arg Ala Ala Ala Ser Val Phe Asp Glu	
20 25 30	
tac ggg ttc gag gcc gcc aca gtg gca gag atc ctc tcg cgg gcc tcg	144
Tyr Gly Phe Glu Ala Ala Thr Val Ala Glu Ile Leu Ser Arg Ala Ser	
35 40 45	
gtc acc aag ggc gcg atg tac ttc cac ttc gct tcc aag gaa gag ctg	192
Val Thr Lys Gly Ala Met Tyr Phe His Phe Ala Ser Lys Glu Glu Leu	
50 55 60	
gcc cgc ggc gtg ctg gcc gag cag acc ctg cac gtg gcg gtg ccg gaa	240
Ala Arg Gly Val Leu Ala Glu Gln Thr Leu His Val Ala Val Pro Glu	
65 70 75 80	
tcc ggc tcc aag gcg cag gaa ctg gta gac ctc acc atg ctg gtc gcc	288
Ser Gly Ser Lys Ala Gln Glu Leu Val Asp Leu Thr Met Leu Val Ala	
85 90 95	
cac ggc atg ctg cac gat ccg atc ctg cgg gcg ggc acg cgg ctc gca	336
His Gly Met Leu His Asp Pro Ile Leu Arg Ala Gly Thr Arg Leu Ala	
100 105 110	
ctg gac cag ggg gcg gtg gac ttc tcc gac gcc aac ccg ttc ggc gag	384
Leu Asp Gln Gly Ala Val Asp Phe Ser Asp Ala Asn Pro Phe Gly Glu	
115 120 125	
tgg ggc gac atc tgc gcc cag ctc ctg gcg gag gca cag gaa cgg ggg	432
Trp Gly Asp Ile Cys Ala Gln Leu Leu Ala Glu Ala Gln Glu Arg Gly	
130 135 140	
gag gtg ctt ccg cac gtg aac ccg aaa aag acc ggc gac ttc atc gtc	480
Glu Val Leu Pro His Val Asn Pro Lys Lys Thr Gly Asp Phe Ile Val	
145 150 155 160	
ggc tgc ttc acc ggg ctc cag gcg gtc tcc cgg gtc acc tcc gac cgc	528
Gly Cys Phe Thr Gly Leu Gln Ala Val Ser Arg Val Thr Ser Asp Arg	
165 170 175	
cag gac ctc ggc cac cgg atc tcg gtg atg tgg aac cac gtg ctg ccc	576
Gln Asp Leu Gly His Arg Ile Ser Val Met Trp Asn His Val Leu Pro	
180 185 190	
agc atc gtg ccg gcg tcc atg ctg acc tgg atc gaa acc ggc gag gag	624
Ser Ile Val Pro Ala Ser Met Leu Thr Trp Ile Glu Thr Gly Glu Glu	
195 200 205	
cgg atc ggg aag gtc gcg gcg gcg gcc gag gcc gcc gag gct gcg gag	672
Arg Ile Gly Lys Val Ala Ala Ala Ala Glu Ala Ala Glu Ala Ala Glu	
210 215 220	
gcc tcc gag gcc gcc tcc gac gag tag	699
Ala Ser Glu Ala Ala Ser Asp Glu	
225 230	

&lt;210&gt; 2

&lt;211&gt; 232

&lt;212&gt; PRT

&lt;213&gt; Streptomyces virginiae

&lt;400&gt; 2

Met Ala Val Arg His Glu Arg Val Ala Val Arg Gln Glu Arg Ala Val  
 1 5 10 15

Arg Thr Arg Gln Ala Ile Val Arg Ala Ala Ala Ser Val Phe Asp Glu  
 20 25 30

Tyr Gly Phe Glu Ala Ala Thr Val Ala Glu Ile Leu Ser Arg Ala Ser  
 35 40 45

Val Thr Lys Gly Ala Met Tyr Phe His Phe Ala Ser Lys Glu Glu Leu  
 50 55 60

Ala Arg Gly Val Leu Ala Glu Gln Thr Leu His Val Ala Val Pro Glu  
 65 70 75 80

Ser Gly Ser Lys Ala Gln Glu Leu Val Asp Leu Thr Met Leu Val Ala  
 85 90 95

His Gly Met Leu His Asp Pro Ile Leu Arg Ala Gly Thr Arg Leu Ala  
 100 105 110

Leu Asp Gln Gly Ala Val Asp Phe Ser Asp Ala Asn Pro Phe Gly Glu  
 115 120 125

Trp Gly Asp Ile Cys Ala Gln Leu Leu Ala Glu Ala Gln Glu Arg Gly  
 130 135 140

Glu Val Leu Pro His Val Asn Pro Lys Lys Thr Gly Asp Phe Ile Val  
 145 150 155 160

Gly Cys Phe Thr Gly Leu Gln Ala Val Ser Arg Val Thr Ser Asp Arg  
 165 170 175

Gln Asp Leu Gly His Arg Ile Ser Val Met Trp Asn His Val Leu Pro  
                   180                                  185                                  190

Ser Ile Val Pro Ala Ser Met Leu Thr Trp Ile Glu Thr Gly Glu Glu  
                   195                                  200                                  205

Arg Ile Gly Lys Val Ala Ala Ala Ala Glu Ala Ala Glu Ala Ala Glu  
                   210                                  215                                  220

Ala Ser Glu Ala Ala Ser Asp Glu  
                   225                                  230

<210> 3

<211> 26

<212> DNA

<213> Streptomyces virginiae

<300>

<301> Kinoshita, H., Tsuji, T., Ipposhi, H., Nihira, T. and Yamada, Y.

<302> Characterization of Binding Sequences for Butyrolactone Autoregulator  
 Receptors in Streptomyces

<303> Journal of Bacteriology

<304> 181

<305> 16

<306> 5075-5080

<307> 1999-08

<308> D32251

<309> 1994-07-19

<313> (1)..(26)

<300>

<301> Kinoshita, H., Tsuji, T., Ipposhi, H., Nihira, T. and Yamada, Y.

<302> Characterization of Binding Sequences for Butyrolactone Autoregulator Receptors in Streptomyces

<303> Journal of Bacteriology

<304> 181

<305> 16

<306> 5075-5080

<307> 1999-08

<308> D32251

<309> 1994-07-19

<400> 3

agatacatat caaccggttc ttttga

26

<210> 4

<211> 110

<212> DNA

<213> Artificial sequence

<220>

<223> Designed sequence of the CamV 35S promoter modified to contain the operator BARE-3 element just downstream of its TAT-box

<400> 4

gatatctcca ctgacgtaag ggatgacgca caatcccact atccttcgca agacccttcc 60

tctatataag agatacatat caaccggttc ttttgacggg ggactctaga 110

<210> 5

<211> 110

<212> DNA

<213> Artificial sequence

<220>

<223> Designed sequence of the CaMV 35S promoter modified to contain the operator BARE-3 element just upstream of its TATA-box

<400> 5

```
gatatctcca ctgacgtaag ggatgacgca caatcagata cataccaacc ggttcttttg      60
actatataag gaagttcatt tcatttgag agaacacggg ggactctaga      110
```

<210> 6

<211> 110

<212> DNA

<213> Artificial sequence

<220>

<223> Designed sequence of the CaMV 35S promoter modified to contain the operator BARE-3 elements just downstream and upstream of its TATA-box

<400> 6

```
gatatctcca ctgacgtaag ggatgacgca caatcagata cataccaacc ggttcttttg      60
actatataag agatacatat caaccggttc ttttgacggg ggactctaga      110
```

<210> 7

<211> 136

<212> DNA

<213> Artificial sequence

<220>

<223> Designed sequence of the CaMV 35S promoter modified to contain three of the operator BARE-3 elements just downstream and upstream of its TATA-box

<400> 7

```
gatatctcca ctgacgtaag ggatgacgca caatcagata cataccaacc ggttcttttg      60
actatataag agatacatac caaccgggttc ttttgaagat acataccaac cggttctttt      120
gacggggggac tctaga                                                         136
```

<210> 8

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> Designed sequence of a backward primer containing the restriction enzyme BamH I recognition sequence for PCR amplification of the barA gene coding region to be cloned by cut with the enzyme

<400> 8

```
taggatccat aaatggcagt gcgacac                                             27
```

<210> 9

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> Designed sequence of a forward primer containing the restriction enzyme Sac I recognition sequence for PCR amplification of the barA gene coding region to be cloned by cut with the enzyme

<400> 9

```
tagagctcct actcgtcgga ggcggcc                                             27
```

<210> 10



<211> 67

<212> DNA

<213> Artificial sequence

<220>

<223> Designed sequence of one of paired oligo DNAs for construction of the modified CaMV 35S promoter containing three of the operator BARE-3 elements just downstream and upstream of its TATA-box

<400> 10

cggatatctc cactgacgta agggatgacg cacaatcaga tacataccaa ccggttcttt 60  
tgactat 67

<210> 11

<211> 89

<212> DNA

<213> Artificial sequence

<220>

<223> Designed sequence of the other of paired oligo DNAs for construction of the modified CaMV 35S promoter containing three of the operator BARE-3 elements just downstream and upstream of its TATA-box

<400> 11

gctctagagt ccccggtcaa aagaaccggt tggatatgtat cttcaaaaga accggttggt 60  
atgtatctct tatatagtca aaagaaccg 89